

(D) OTHER INFORMATION: /note= "N = C, A, T or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

5 GGGCTACTTG AAAGGGACAT TCCTTCGTTT NNNATTCTG GATTTGAAGT ACCCC 55

(2) INFORMATION FOR SEQ ID NO:54:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCATTTAAAG AATGGGAAGT AGATCCTAAT AATCCTGGAA CCAGGACCAG AGTAATTGAT 60

20 CGC 63

(2) INFORMATION FOR SEQ ID NO:55:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val Asp Pro Asn Asn Pro Gly
1 5

35 (2) INFORMATION FOR SEQ ID NO:56:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCATTTAAAG AATGGGAAGA AGATCCCCAT AATCCAGCAA CCAGGACCAG AGTAATTGAT 60

CGC 63

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(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Asp Pro His Asn Pro Ala
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(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

48

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AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

96

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TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC
 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

144

40

TTT GTA CCA GGG GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG
 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

192

45

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

240

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CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT
 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

288

GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA
 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

336

	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	115 120 125	384
5	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	130 135 140	432
10	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	145 150 155 160	480
15	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	165 170 175	528
20	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	180 185 190	576
25	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	195 200 205	624
30	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG GCT AGC ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp	210 215 220	672
35	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	225 230 235 240	720
40	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	245 250 255	768
45	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	260 265 270	816
50	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	275 280 285	864
	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	290 295 300	912
	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	305 310 315 320	960